Editorial

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Advancements in mass spectrometry as a tool for clinical analysis: part II

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Welcome to the second and final part of the special issue on *Advancements in Mass Spectrometry as a Tool for Clinical Analysis*. Part I addressed perhaps the more traditional themes of mass spectrometry (MS) in the clinical laboratory, notably for toxicological assessments and quantitative analysis of small molecules [1]. In this, part II, we diverge our interests into complex biological profiling, including large protein analyses as well as discovery-based 'omics investigations. We will also consider the current and future potential of MS in imaging science. Finally, we gain some insight into the possibility of automated MS for clinical workflows. The four main themes included in this issue are:

Quantitative protein assessment

Assessment of protein levels for clinical workflows has long been performed using immunometric, turbidimetric and nephelometric techniques, typically performed by a multi-purpose clinical chemistry autoanalyzer [2, 3]. Measurement of specific proteins by MS can require extensive development, most notably when considering the behavior of and interferences to intact proteins in both the chromatographic and ionization spaces [4]. Nonetheless, the specificity provided by MS offers huge potential to explore the extensive complexity of the human proteome [5], as well for the development and measurement of novel protein biomarkers. Nedelkov and Yu [6] showcase some of the advantages of MS with discussion of apolipoprotein C-III proteoform measurements. This is followed by two original research articles. The first addresses the improved measurement of therapeutic monoclonal antibodies applying a middle-up protein subunit approach [7]. The second demonstrates the potential application of inductively coupled plasma-MS (ICP-MS) for clinical

measurement of carcinoembryonic antigen through a europium-tagged immunolabeling approach [8].

MALDI-MS for the clinic

Matrix-assisted laser desorption ionization-MS, or commonly known as MALDI-MS, has been the subject of increasing interest over recent years, mainly owing to the improvements in mass spectral and spatial resolution afforded by modern instrumentation. In this section, we present three review articles that discuss the potential for MALDI-MS as a routine clinical biomarker technology [9], alongside its applications as an imaging technique for fracture healing [10] and cellular-level measurements [11]. In addition to these, Lellmen and Cramer [12] present original research into the application of liquid atmospheric pressure-MALDI-MS to identify bacteria based on the measurement of unique lipid profiles.

Clinical application of 'omics technologies

MS has afforded a wide range of new applications that have expanded on traditional 'omics technologies, such as those used for genomic sequencing [13]. In this section, we begin with Dr. Misra discussing his thoughts and views on the potential pathways and hurdles for use of an individualized metabolomics approach for clinical biomarker measurements [14]. Further opinion pieces are then presented for discussion on clinical proteomic amyloid typing [15], and within the interesting field of the human volatilome and the potential to combine canine and electronic 'sniffing devices' for clinical monitoring [16]. These thought-provoking opinion articles are supported by original research investigations into

the utility of proteomics in the diagnosis of inflammatory bowel diseases [17], and the exploration of prostate cancer biology [18].

Laboratory automation and kit-based approaches

MS is a complex field and acquiring expertise in the development and application of biomarker assays requires many years of advanced training. The talented pool of scientists knowledgeable in MS cannot be replaced entirely by non-expert users. However, the field is working toward streamlining and improving reproducibility for repeated laboratory protocols using automated processes. Salvagno et al. [19] discuss the opportunities and challenges faced with the prospect of automated MS analyses, with additional comments from Le Goff and colleagues [20] regarding the pros and cons of applying MS processes with homemade or ready-to-use kit-based approaches. Finally, this section is rounded up with the investigation into the use of a fully automated liquid chromatography (LC)-MS system for 25-hydroxy vitamin D measurements [21].

This concludes the special issue on MS. It has been a delight to serve as Guest Editor for this project and I would like to again thank the authors and reviewers for their time and efforts. We sincerely hope you enjoy the articles published in this special issue. I encourage all who perform research in clinical MS to continue the excellent progress being made, and eagerly encourage readers to submit their future work to *Clinical Chemistry and Laboratory Medicine*.

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