A mass spectrometry view into diverse aspects of glycobiology

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Abstract

Around for more than a century, the analytical technique of mass spectrometry is blooming more than ever, and applied in nearly all aspects of the natural and life sciences. In the last two decades mass spectrometry has become routine for the high-throughput analysis of peptides and glycans, and to a lesser extent glycopeptides. However, also intact proteins and even complete protein complexes can nowadays be analyzed. In this lecture, I will describe the emerging role of mass spectrometry with its different technical facets in molecular and structural biology, focusing especially on the analysis of intact glycoproteins. Moreover, I will describe how we use native mass spectrometry to study dynamic protein assemblies, for instance those involved in complement activation.

Recent developments in mass spectrometry technology have allowed us to analyze intact native glycoproteins and protein complexes using Q-ToF and Orbitrap mass analyzers with very high sensitivity and mass resolving power, enabling us to profile the quality and biosimilarity of protein biotherapeutics, in their native state without requiring much sample preparation. In detail, I will demonstrate how native mass spectrometry can be combined with middle-down proteomics to profile complex structures of various glycoproteins, focusing on mAbs, Erythropoietin and plasma proteins. Thereby I will address the question of how unique each person is, as viewed from each individual’s glycoproteome.

Biography

Albert J.R. Heck (1964) of Utrecht University is scientific director of the Netherlands Proteomics Centre. Heck’s group emphasizes on the development and applications of advanced mass spectrometry-based proteomics technologies. Heck’s proteomics research focuses for a large part on cancer, stem cells and immunology. Besides the proteomics efforts, the group of Heck is also well known for its expertise in mass spectrometry based structural biology, using native mass spectrometry, cross-linking and/or HD exchange mass spectrometry. Heck is recipient of awards such as the HUPO Discovery Award (2013), and the Proteomics Pioneer Award from the European Proteomics Association (EuPA, 2014). In 2016 he received the ACS Frank H. Field and Joe L. Franklin Award. In 2014 he became elected member of EMBO and the Royal Netherlands Academy of Sciences and Arts (KNAW). In 2017 Heck received the Spinoza Prize, the most distinguished scientific award in the Netherlands. In 2018 Heck received the Thomson medal of the International Mass Spectrometry Society and the Krebs medal (FEBS). In his recent work Heck is focusing on what he terms proteome and proteoform diversity and develops new technologies to expose and quantify such features by hybrid mass spectrometry approaches.