Focus on Proteomics in Honor of Ruedi Aebersold, 2002 Biemann Awardee

It is a pleasure to introduce this series of articles honouring the achievements of Ruedi Aebersold, the 2002 recipient of the ASMS Biemann Medal. During the last decade enormous progress has been made in the application of mass spectrometry to proteomics, an area to which Ruedi has contributed both generally and specifically with his isotope labelling strategies. In his opening Account and Perspective, "A Mass Spectrometric Journey into Protein and Proteome Research," Ruedi poses the interesting question 'does technology drive biology or is the converse the case, where the biological question drives the technological development?' This of course remains an open question but the accompanying series of articles exemplify the tremendous synergy between biology and methodological development.

An important biological question prompts the first of the research articles; "Quantitative Proteomic Analysis of Chromatin-associated Factors" by Yuzuru Shiio, Eugene C. Yi, Sam Donohoe, David R. Goodlett, Ruedi Aebersold, and Robert N. Eisenman. A method is described for determining quantitatively the changes in chromatin-associated factors. These factors play a central role in cell proliferation, differentiation and death and yet are difficult to quantify primarily due to their very low levels of expression. The method that is described is based on the ICAT methodology, which Ruedi pioneered. On the same theme, the next article

"Trypsin Catalyzed ^{16}O -to- ^{18}O Exchange for Comparative Proteomics: Tandem Mass Spectrometry Comparison using MALDI-TOF, ESI-QTOF and ESI-Ion Trap Mass Spectrometers" by Manfred Heller, Hassan Mat-tou, Christoph Menzel, and Xudong Yao illustrates the use of alternative labeling strategies involving ^{16}O to ^{18}O , in conjunction with enzymatic digestion for identifying proteins in human plasma. Of additional interest in this article is the comparison of the many different mass spectrometry platforms emerging for analysing such data including LC MALDI MS/MS approaches.

Chromatographic separation is at the heart of many successful proteomic strategies, and an alternative approach is exemplified by Figeys and colleagues in their article, "On-line Strong Cation Exchange μ -HPLC-ESI-MS/MS for Protein Identification and Process Optimization." Using a strong cation exchange micro LC method for identification of proteins in mixtures, they apply their approach to a tryptic digest of a protein extract from human cells. They demonstrate that their procedure provides complementary information to standard reverse phase chromatographic methods, specifically for larger molecular-weight peptides that are often poorly represented using standard protocols.

An exciting biological challenge involves definition of the protein composition of the editosome, a multi-protein complex involved in editing mitochondrial mRNAs in trypanosomes. This subject, which is described by Aswini K. Panigrahi, Thomas E. Allen, Paul

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A. Haynes, Steven P. Gygi, and Kenneth Stuart in “Mass Spectrometric Analysis of the Editosome and Other Multiprotein Complexes in *Trypanosoma brucei*,” provides an excellent example of a proteomics approach to defining functional complexes. The results reveal candidate proteins of the editosome as well as the identity of other novel mitochondrial proteins.

On a similar theme, the identity of proteins from an unknown plant virus illustrates a novel application of a proteomics approach. Starting with the uninfected tobacco plant and comparison of the protein components with that of a plant infected with tobacco mosaic virus, Haynes et al in their article “Investigative Proteomics: Identification of an Unknown Plant Virus from Infected Plants Using Mass Spectrometry” demonstrated the principle of the experiment. After separation protein spots that were differentially expressed were identified. The approach was then applied to identify an unknown virus revealing proteins of the potato virus X.

The final article, “Proteomic Analysis of *Pseudomonas aeruginosa* Grown Under Magnesium Limitation” by Tina Guina, Manhong Wu, Samuel O. Purvine, Eugene C. Yi, Robert K. Ernst, Kimberly A. Lee, Jimmy Eng,

David R. Goodlett, Ruedi Aebersold, and Samuel I. Miller demonstrates a quantitative approach to the proteomic analysis of a microorganism, grown under specific conditions. Here the labeling strategy devised by Ruedi is used to good effect illustrating its application for large-scale quantitative proteomics.

This collection of articles exemplify how in some studies, biology is the major driving force, as is perhaps the case for the quantification of chromatin-associated factors, definition of the editosome or identification of a virus. In others, the methodological development is the key component, in the form of different chromatographic strategies, quantification of the phosphoproteome, or refinements of the isotope labelling strategies. In either case, the impact is significant. Consequently, whatever the stimulus, the results from these investigations have important implications and are changing the ways in which biological research is conducted, now and for the foreseeable future.

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