Focus on Industrial Proteomics: Dedicated to the late Dr. Robert S. Bordoli

Mass spectrometry together with appropriate separation techniques is playing a major role in proteomics. The literature reflects the substantial contribution made to mass spectrometry and proteomics by academic institutions. Industrial applications, particular from pharmaceutical companies, are less widely reported but are often the driving force for high throughput approaches and automation. With increasing complexity of mixtures and requirement for high throughput strategies comes the need for greater mass accuracy and sensitivity. This has often provided the stimulus for novel instrumentation. The aims behind this focus on industrial proteomics are therefore two-fold: to highlight recent developments in commercial instrumentation and to provide an opportunity for pharmaceutical companies to report recent advances in methodology.

The analysis of very complex mixtures of proteins under robust automation is key to high throughput proteomic strategies. In the first of these articles the problems encountered with analyzing complex protein mixtures using LC-MS approaches are tackled by Vissers and colleagues. Obtaining high quality mass spectra of multiple components is often difficult under conditions used for chromatographic separation due to fast flow rates. By varying the flow such that components of interest can be analyzed at a lower rate than the bulk solution, optimal MS/MS spectra have been acquired. The procedure is compatible with automation and demonstrated in the analysis of ribosomal proteins.

Since proteomics is often the major driving force behind the design of new instrumentation two recent developments are reported in the focus issue. A MALDI Q-TOF instrument was evaluated by Wattenberg and colleagues using standard peptides and compared with nanoelectrospray data. The MALDI Q-TOF data reveal regular b- and y- type ions, as in the nanoelectrospray spectra but in addition, a- type ions are also observed. For a MALDI TOF -TOF instrument, Yergey et al. show fragmentation spectra collected in two different modes, via metastable decomposition and collision-induced dissociation. The combination of these fragmentation spectra increase the level of sequence information available and is demonstrated by de novo sequencing of peptide mixtures extracted from a sea urchin protein.

One of the major drawbacks to the quadrupole time-of-flight methodology has been the absence of neutral loss and parent ion scans, commonly used to identify post-translational modifications in triple quadrupole and magnetic sector instruments. One approach to overcome this apparent shortfall is presented by Bateman and colleagues. A method is described involving programming of a Q-TOF instrument to recognize specific fragments and record product ion spectra within the timescale of the evolution of a chromotagraphic peak. The technique is demonstrated by identifying phosphorylated components from a complex mixture of peptides generated by digestion from beta-casein.

The unambiguous identification of whole proteins from organisms remains a formidable task. One constraint that could be imposed is to label specific residues providing data for discriminating possible assignments. Using this approach, Ogorzalek-Loo and colleagues demonstrate that by stressing a culture and simultaneously labeling cysteine residues, it is possible to assess the cell's response to the perturbation. The method was used to identify differential expression of a stress protein in response to an antibacterial agent.

The articles in this focus on industrial proteomics are dedicated to the memory of Robert S. Bordoli who died on 24th October 2000, at the age of 47. During his lifetime Bob made many significant contributions to mass spectrometry. His early days at the University of Manchester Institute of Science and Technology (UMIST) were spent working with Micky Barber on the first demonstrations of the fast atom bombardment source for organic mass spectrometry. He then began working for Micromass and contributed to the devolvement and application of sector instruments. In January 1996 Bob began using a prototype Q-TOF mass spectrometer and to focus on the emerging role of mass spectrometry in proteomics. In 1997, at the ASMS meeting in Palm Springs, he presented recent peptide sequencing results from the Q-TOF. It was also at that meeting that Bob first became aware of the possibility that he had melanoma.

Bob was very well known in the field of mass spectrometry. He was always keen to collaborate and his infectious enthusiasm and humor inspired many scientists. Two of the contributions in this focus issue were carried out in association with Bob and although it is now 18 months since he died, he is still sadly missed by all who knew him.

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