Mind the technology gap

A special Focus (beginning on p. 781) on mass spectrometry in proteomics applications is intended to inspire more cell biologists to take advantage of this powerful technology.

Once upon a time, which was actually not all that long ago, sequencing the human genome was a Herculean task. But it was a worthy goal, and its success has had far-reaching implications, from enabling new fields in biology to the dawn of personalized medicine.

Now in the post-genomic era, a large part of the spotlight has turned to proteins. The proteome, however, is a much more complex entity than the relatively static genome; protein composition, expression levels, interactions and post-translational modifications are constantly changing. As such, analyzing the proteome is a massive experimental challenge. But mass-spectrometry technology, sample-preparation methods and data-analysis tools have been advancing by leaps and bounds in recent years. Mass spectrometry has matured into the most powerful technology currently available to proteomics researchers both in terms of its high-throughput capacity and the range of molecular information that can be gleaned from it. It is an incredibly useful tool for biology that offers much more than just the ability to generate 'parts lists'. Mass spectrometry approaches have led to important insights in such endeavors as defining the protein composition of cellular organelles, localizing sites of post-translational modifications on proteins involved in cellular signaling and mapping protein-interaction networks.

But, for all of its potential, mass spectrometry–based proteomics still remains a somewhat isolated field, and mass spectrometry has not been routinely incorporated as a tool in more traditional cell biology research. Historically, mass spectrometry has been a chemist's tool and only recently has it been applied to address biological questions. Therefore, it has not been traditionally taught in biology curriculums, and many biologists are never exposed to this fairly complex technique during their training. Some other reasons that have perhaps discouraged biologists to bridge this 'technology gap' are explored in a Commentary by John Bergeron and colleagues (p. 783).

Mass spectrometry-based proteomics may also suffer from the same mistrust that affects other high-throughput technologies, stemming from the potential for false positives and false negatives as well as the ever-growing impossibility of following up with comprehensive validation, one protein at a time. Precisely for these reasons much effort has been invested in developing robust statistical methods to assess and ensure the quality of results. On page 787, Ruedi Aebersold and colleagues review the most important approaches and computational tools for data analysis.

Another hurdle is the issue of how best to represent the huge amounts of proteomics data to facilitate data sharing and minimize error propagation. The proteomics field is aware of this issue, and dedicated individuals are making strides to address it; the Human Proteome Organization Proteomics Standards Initiative recently published its MIAPE standards outlining the 'minimum information about a proteomics experiment' that should be reported when publishing proteomics data (see Research Highlight on p. 774). This first step toward standardizing the reporting of proteomics data will hopefully lead to its improved annotation in databases. A practical issue also arises in dealing with a plethora of data formats, as well as the burden placed on researchers to deposit data. Careful data annotation and deposition, however, greatly benefit both the data producers and the data consumers. With reporting standards and appropriate databases now available, *Nature Methods* will strongly encourage the deposition of all proteomics data into publicly available databases.

Mass spectrometry also has the potential to be a powerful tool for clinical applications, most notably for the discovery of biomarkers for early detection of diseases. Despite the early hype, however, no reliable diagnostic test has yet been developed based on mass spectrometry, and the field has taken a psychological hit as a result. In a Commentary on page 785, Laura Beretta discusses the specific challenges that the clinical proteomics field faces and outlines a realistic path to continue to advance the field forward.

Clearly, it will take a team effort between mass spectrometrists, cell biologists, clinicians and bioinformaticians to make mass spectrometry a routine tool in cell biology research as well as in the clinic. In this Focus issue, we invited several researchers who have managed to bridge this technology gap to contribute their expertise as well as their visions for the future of mass spectrometry in biology. We hope that these Commentaries, Reviews and Perspectives will inspire more biologists to explore and to help advance this promising and powerful technology.