High resolution biopolymer mass spectrometry: new perspectives for analysis of complex biological mixtures and combinatorial libraries

Michael Przybylski
Department of Chemistry, Analytical Chemistry, University of Konstanz, D-78457 Konstanz, Germany

The development of efficient "soft ionisation" methods in the last years has provided the basis for the molecular characterisation of biopolymers by mass spectrometry. In contrast to previous limitations in the molecular weight range amenable, electrospray ionisation (ESI-MS) and matrix assisted laser desorption ionisation (MALDI-MS) have provided access to biopolymers >> 100 kDa. The recent development of Fourier transform ion cyclotron resonance (FTICR) mass spectrometry enabled a breakthrough for the ultra-high resolution mass spectrometric analysis of biopolymers using both ESI and MALDI ionisation [1]. Present studies in our laboratory on the analytical development of ESI-FTICR mass spectrometry focus on (i) the structure analysis of non-covalent supramolecular biopolymer complexes [2]; (ii) direct, high resolution mass spectrometry of peptide mixtures in proteome analysis and analysis of combinatorial mixtures; and (iii) the identification of antigenic determinant structures of mono- and polyclonal antibodies using mass spectrometric epitope mapping methods [3,4]. Recent applications of FTICR-MS to proteome studies of target antigens for auto-immune diseases will be discussed. In these studies a new approach ("affinity proteomics") has been developed with which FTICR-MS is providing unprecendented identification selectivity for proteins from complex biological mixtures. [5]

[1] A.G. Marshall (1998) *Mass Spectrom. Rev.* **17**, 1.

[2] M. Przybylski et al. (1998) in "*New Methods for the Study of Biomolecular Complexes", (W. Ens, ed.),* Kluwer Acad. Publ., Amsterdam, 17-43.

[3] M. Przybylski (1995), *Adv. Mass Spectrom.* **13**, 257-283.

[4] M. Macht, W. Fiedler, K. Kürzinger, M. Przybylski (1996) *Biochemistry***35**, 15633-15638.

[5] M. Kohlmann, M. Macht, S. Deininger, A. Marquardt, M. Przybylski (2001) *Science*, in press.