

Foreword

The 21st Montreux LC–MS symposium was held from 10 to 12 November 2004 in Montreux, Switzerland. The continuously growing field of LC–MS was reflected by the over 30 nationalities attending the conference and again a growth in scientific contributions from a variety of research and development domains such as pharmaceutical, biotechnological, food, environmental and research on novel instrumentation.

The novel developments in mass spectrometry and separation science have considerable impact on novel application areas by generating more information or enabling much faster experimentation. The opening of the symposium given by Professor Don Hunt was an example of how novel instrumentation using a combination of linear ion trap technology and FT–MS yields a robust high resolution setup to explore novel cutting edge biology questions related to discovery of new elements in the histone code, immunology, cancer vaccine and biomarker research. The new presented electron transfer dissociation technology to compliment collision-activated dissociation (CAD) or perhaps replacing it in the peptide analysis, underlined novel opportunities evolving from new instrumental achievements.

High resolution combined with high mass accuracy obtained via different hybrid technologies clearly demonstrate the importance for solving various problems in the LC–MS field of which several elegant applications were demonstrated in proteomics and metabolomics research. Varieties of combinations with different separation strategies enable novel strategies. Research focusing on fast separations uses on the one hand, high flow approaches like (parallel) turbulent flow and monolithic based columns in quantitative bioanalysis or ultra-performance liquid chromatography (UPLC) for efficient profiling of endogenous metabolites (metabolomics). On the other hand, miniaturization becomes more and more a driver for situations where sample volumes are limited or when high sensitivity is aimed for applying nano-electrospray and chip-based approaches. Various chip-based designs including highly automated approaches are clearly indicating the acceptance of these designs in Research and Development laboratories. Single cell analysis or compartmental cell

analysis is coming closer when combining further miniaturized electrospray (pico/femto-electrospray) and sample/cell handling based also on chip designs. Also miniaturized LC as in nano-LC continues to deliver impressive separation and sensitivity characteristics.

In complex cases electromigration technologies provide a good basis not only for chip-based technologies, but also for impurity profiling using atmospheric pressure photo ionization as was demonstrated for coupling of CE or micellar electrokinetic chromatography with mass spectrometry. In addition, multidimensional LC strategies remain an important strategy in proteomics research but covering the enormous dynamic range is still a challenge. Sample preparation is still limiting in most cases and continuing research in this area will greatly enhance the overall performance of the LC–MS systems. Impressive results were presented using multidimensional solid-phase extraction yielding five-dimensional sample clean-up with complete reduction of ion suppression for direct injection of body fluids combined with high selectivity for the window of the target class of components.

The high productivity of LC–MS systems in case of profiling strategies create higher demands on the evaluating software, such as pattern recognition techniques and several interesting approaches are emerging more and more, addressing special mass spectrometric aspects as encountered in data pre-processing including peak alignment and peak picking, but especially software specialized for identification strategies have regained interest for biomarker discovery. Several contributions were aiming on improving the identification addressing the informatively, reproducibility and specificity aspects of different ionization methods in combination with LC–multiple MS spectra.

The LC–MS field clearly continues to grow in all domains and more novel breakthroughs can be expected in near future research, making it one of the most exciting areas within analytical sciences and biological research.

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