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Journal of Chromatography A, 1020 (2003) 1

JOURNAL OF
CHROMATOGRAPHY A

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Foreword

The 19th Montreux symposium was held from 6 to 8 November 2002 and the formula of short courses, an exciting scientific program and exhibition covering all major vendors with the latest developments was again very successful. The overall attendance was around 750 persons, which was a further increase compared to the 2000 meeting.

Although LC–MS has become a mature technology, the field is still very innovative in development of technologies and applied methodology which was reflected in numerous posters and presentations.

An important new direction was discussed in the opening lecture of the symposium by Dave Clemmer addressing LC–ion mobility technology for peptides/proteins, demonstrating the extended profiling capacity of such hyphenation. The complexity of biological systems is a general guide for the development of techniques being able to measure many components simultaneously—profiling or fingerprinting—most notably in proteomics, metabolomics or the integration via systems biology. Hyphenated techniques play a major role and will be the core technology for new discovery platforms in biology within life sciences. Focus is strongly on biomarker detection related to diseases and biomarker profiling related to drug response or nutritional interventions. Several contributions highlighted this important trend and also revealed the crucial component for these new directions namely the software based on a mixture of data pre-processing, biostatistics, archival strategies and bioinformatics. The fast amount of data generated by modern instrumentation in analyzing biological samples needs sophisticated strategies to transfer data into information and finally into knowledge.

In general terms new highlights in instrumentation and methods were reflected in contributions on LC/CE–FT–MS, parallel evaporative light scattering detection, monolithic capillary columns, linear ion traps, high-resolution time-of-flight and triple quadrupole measurements, SALDI–MS, matrix-assisted laser desorption ionization ion trap, and a series of miniaturization based or chip-based advances in LC–MS. The aspect of miniaturization based on limited sample availability was addressed in various contributions and the trend continues to move into this direction. Integrated in all applications is the challenge of sample preparation to cover a wide dynamic range, allowing reliable quantitation by removing among other ion suppression effects. Multi-dimensional chromatography or special stationary phases dominate the advanced approaches. Although identification has been a major asset of all mass spectrometry based hyphenated methodologies, it is clear that after an enormous focus on quantitation and throughput in the last decade new identification strategies are gaining attention again. This implies that in addition to MS–MS techniques high resolution measurements are more emphasized again and in this respect FT–MS is moving forward in an attractive way to become a more robust methodology for routine analytical investigations.

The symposium series reflects the enormous growth in mass spectrometry as a tool in the life sciences and all indications are extremely positive for continuation of this trend.

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