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Foreword

From a slow and relatively unpromising start (as anyone who tried to use early devices such as the moving belt and direct liquid introduction interfaces etc., will remember), the successful coupling of HPLC with MS has come to represent the very acme of sensitive and specific analytical techniques. Indeed it is arguable that the recent advances that we have observed in the area of the hyphenation of LC–MS represent one of the finest achievements of late 20th century analytical science. Given the transformation of bioanalysis as a result of HPLC–MS and MS–MS, it is now difficult to contemplate drug analysis in complex matrices such as plasma and urine without access to this remarkable technology. These advances demanded much skill and dedication and required the involvement of many scientists and instrument designers in order for them to happen. So to mark these advances, and to note in passing the end of one millenium and the beginning of another, we have chosen to produce a special issue of the Journal of Chromatography B, centered on HPLC–MS and related techniques. This was done with the intention of celebrating the advances and to honour the achievements of Prof. Fred W. McLafferty, one of the pioneers of mass spectrometry.

Born in 1923, Prof. McLafferty has had a remarkable career in mass spectrometry in fields such as gaseous ion reactions (notably the McLafferty rearrangement); instrumentation such as GC–MS, HPLC–MS, and HPLC–MS–MS; special techniques such as collisionally activated dissociation, neutralisation-reionisation and electron capture dissociation; computer data acquisition, reduction and identification via probability-based matching and high resolution MS–MS characterisation of biomolecules. This research has resulted in over 450 publications

including works such as “Mass Spectrometry of Organic ions”, “Mass Spectral Correlations”, “Interpretation of Mass Spectra” and “Tandem Mass Spectrometry”. In addition he has been involved as an editor and editorial advisory board member on many journals. His work has brought him many honours and awards from learned societies all over the world. I particularly remember the award of the Robert Boyle Gold Medal from the Analytical Division of the Royal Society of Chemistry in 1992 where the lecture he gave, and the enthusiasm with which it was delivered, brought to life the possibilities that LC–MS and ion traps, etc., offered to me as a chromatographer. All of this promise has now been delivered in full measure, as the papers in this special issue show, covering as they do a wide range of techniques and applications of the hyphenation of separations to MS. In addition to honouring the career and contributions of Prof. McLafferty we also wish to extend our thanks as chromatographers and bioanalysts to the countless other individuals who have made these tools available to us.

In addition, in this volume we have tried to point to future possibilities in the hyphenation of spectroscopy with chromatography. Whilst HPLC–MS–MS is currently without question the preeminent technique for quantification it is also used for the characterisation and identification of unknowns. However, we all know from experience that for the purposes of identification MS is not always sufficient. Another recent advance in the area of hyphenation for identification is HPLC–NMR which provides complimentary information. Although unlikely ever to be as widely used as HPLC–MS it is nevertheless becoming more popular, as is the double hyphenation of HPLC–NMR–MS. We have

therefore sought to include in this special issue papers that show how the HPLC–MS, HPLC–NMR and HPLC–NMR–MS can be used together to solve problems.

It is difficult to predict the future with any accuracy (at least until after it has happened),

however, there can be no doubt that the rapid, and continuing, evolution that we have experienced in HPLC–MS in the last decade has made it an exciting time to be a bioanalyst.

Ian D. Wilson