

Obituary

Robert S. Bordoli

(1953-2001)

Following his BSc degree from UMIST in 1974, Bob Bordoli did a PhD with John Vickerman on the use of Static Secondary Ion Mass Spectrometry to probe the surface chemistry of solids. As part of this work that led to the development of a Fast Atom Bombardment (FAB) Quadrupole Mass Spectrometer (*J. Chem Soc. Chem. Commun.* **1981**, 324-325), Bob built the first fast atom beam system for SIMS. His thesis was examined by Allan Maccoll.

Bob then worked as a post-doctoral fellow with Mickey Barber and Don Sedgwick on the development of the first FAB source for organic mass spectrometry. This prototype was fitted on a modified AEI MS902 soon to be followed, through collaboration with Brian Green, with a commercial version on a reversed geometry VG ZAB-HF. The group then proceeded to use FAB to obtain mass spectra from a range of hitherto intractable species (*J. Chem Soc. Chem. Commun.* **1981**, 325-327). The FAB technique led to a renaissance in mass spectrometry as it provided non-thermally induced structurally related fragmentation and ready access to metastable information through 1st and 2nd field free fragmentations on the MS902, and MIKES on the ZAB-HF. Now, molecules of biological interest could be studied without the need for pre-treatment and FAB MS became a key analytical technique for biochemists. The paper on FAB by Barber, Bordoli, Sedgwick and Tyler contained a prophetic statement on "the inadequacies of most mass spectrometers in terms of their energy focusing and ion source extraction of the high masses which this new ion source now makes possible". Overcoming these problems, especially for the study of biological molecules, was the single theme that dominated the remainder of Bob's career and this was a task to which Bob's special combination of instrument development expertise and chemical problem solving ability made him uniquely suited.

In 1983, Bob joined VG Analytical as a development scientist, becoming involved with the development of magnetic sector instruments with improved mass range and greater sensitivity. He also evaluated the ZAB-4F, the first commercial four sector MS/MS system, for the structural determination of biological molecules ionised by FAB. With Mickey Barber and Brian Green he started to learn the rules for interpretation of MS/MS spectra of peptides. He then became involved with the development of the ZAB-SE, with a mass range of 15,000 at full sensitivity, and the ZABSE-4F, probably the longest ever commercial mass spectrometer! In all this work he never lost sight of the need to use the instruments to solve real problems arising from the practice of biological chemistry.

Bob made such an impact with this work that he was appointed Managing Director of one of the VG companies in which post he spent about two years before a corporate reorganisation got him back to the science that he enjoyed most. At this stage Bob became product manager for the AutoSpec, moving later to the AutoSpec-T, the tandem 'four-sector' MS/MS system with array detector. He then worked on the development of the array detector on the AutoSpec-FPD, the development of the ZabSpec-T 'four-sector' MS/MS instrument, the ZabSpec-FPD focal plane detector instrument, and the ZabSpec-Ultima, a 120,000 resolution version of the ZabSpec. This was followed by his involvement in the development of the Q-TOF series of instruments and in using the instruments to solve biological problems. Once again he was showing his ability to drive forward biological chemistry with the help of MS and to drive forward mass spectrometry instrument development through his interest in biochemical problem solving. Bob used the prototype Q-TOF for the analysis of biological samples by MS/MS, and he presented the first results from the Q-TOF at the 1996 ASMS meeting in Portland and co-authored the first paper on it (*Rapid Commun. Mass Spectrom.* **1996**, 10, 889). Bob then focussed on the emerging role of MS in proteomics, and was involved in co-ordinating his company's approach to this application, encompassing MALDI, nanoflow LC-MS and MS/MS on the Q-TOF, and the extensive use of software. He was particularly involved in the evaluation of the new maximum entropy software for de-novo sequencing of peptides, and also helped develop the MALDI source on the Q-TOF.

Bob's industrial career led to over 50 published papers and to numerous conference contributions, in addition to the many papers that had resulted from his UMIST career. He was an excellent lecturer and, as a result, he became in many ways the face of his company to the scientific community. Bob died peacefully at home in 2000 at the age of 47, as a result of a recurrence of a cancer that first attacked him in 1997. The BMSS (with support from Waters) has honoured him by naming its prize for the best young persons' poster presentation at the Annual Conference, the Bordoli Prize

From John Monaghan's article in *BMSS Mass Matters* April 2006

