FOCUS: MS/MS PEPTIDE IDENTIFICATION: EDITORIAL

Focus in Honor of Béla Paizs, Recipient of the 2011 Biemann Medal

The 2011 Biemann Medal was presented to Dr. Béla Paizs at the 59th ASMS Conference for his seminal contributions to a comprehensive understanding of peptide ion fragmentation. Tandem mass spectrometric analysis of peptides, a vital element of proteomics, requires a full analysis of the complex fragmentation reaction networks occurring in mass spectrometers under various excitation conditions. The focused efforts of Béla Paizs have led to detailed characterization of peptide fragment ion structures and dissociation mechanisms, and have demonstrated that the principal characteristics of the collision-induced dissociation spectra of peptides can be understood with fundamental physical and chemical principles. Béla's work combines various experimental techniques (e.g., MS/MS, "action" infrared multiphoton dissociation, ion mobility spectrometry, gas-phase H/D-exchange) with state-of-the-art theoretical methods. "Raw" experimental data (fragmentation patterns, IR spectra, collision cross-sections, etc.) are processed with the help of advanced modeling and provide invaluable structural, thermodynamic, and kinetic data on peptide fragmentation chemistry. Among other achievements, Béla has characterized the major fragmentation pathways leading to **b**, **y**, and **a** ions, the scrambling chemistry of **b** fragments, and, very recently, he has described a new rearrangement pathway for **a** fragments. His work has unified diverse dissociation mechanisms into a comprehensive peptide fragmentation model. These achievements have substantially advanced the field of peptide characterization and provide a solid scientific background for developing improved bioinformatics tools for peptide sequencing in mainstream proteomics.

Béla received his Ph.D. in Chemistry in 1998 from Eötvös University in Budapest, Hungary, and graduated with *summa cum laude* honors. He served as a postdoctoral fellow in the Department of Molecular Biophysics and later in the National Genome Research Network Protein Analysis Facility, DKFZ, Heidelberg, Germany. Between 2004 and 2009, Béla was Group Leader of the Gas-Phase Peptide Chemistry Group in the Department of Molecular Biophysics at the German Cancer Research Center in Heidelberg. Since September 2009, he has been serving as Group Leader of the Computational Proteomics Group of the German Cancer Research Center. Béla has published 70 refereed papers in

prestigious journals, including 14 papers in *JASMS*, and a high impact review (*Mass Spec. Rev.* **24**, 508, 2005), which has received 350 citations.

Béla is an exceptionally active ASMS member and contributor. He is co-founder of the Peptide Fragmentation Interest Group and organized successful workshops at the annual ASMS conferences from 2008 to 2010. In 2011 he co-chaired the ASMS Sanibel Conference on peptide fragmentation and sequencing that brought together scientists active in fragmentation chemistry and MS-related bioinformatics. In addition, he co-edited a focus issue on peptide fragmentation for *JASMS* in 2008 and is now serving on the Editorial Board of the society journal.

The editors of the *Journal of the American Society for Mass Spectrometry* are pleased to dedicate this Special

Focus Issue to Béla Paizs. This issue highlights recent work from Béla's group as well as eight papers from leading researchers in the field. The first article, by Gavin Reid and co-workers, describes an amine specific peptide derivatization strategy that uses novel fixed charge sulfonium ion reagents encoded with isobaric stable isotopes; this approach, coupled with a data-dependent analysis strategy, provides enhanced phosphopeptide quantitation, identification, and phosphorylation site characterization. The contribution by Alex Harrison describes the fragmentation of ions derived from amides containing proline. The production mass spectra of three b_5 ions indicate macrocyclization/reopening to produce a common mixture of intermediates prior to fragmentation; in contrast, the results for a_5 ions indicate significant differences in the mixture of classical substituted iminium ions and protonated C-terminal amides formed by cyclization/rearrangement. The article by Katalin Medzihradszky and Jonathan Trinidad explores the unusual CID fragmentation of Pro-Ser/Thr-containing peptides; accurate mass measurements indicate elimination of phosphoric acid followed by fragmentation between the α -carbon and the carbonyl group of the proline residue. The paper of Frantisek Turecek and co-authors describes tunable charge tags for electron-based methods of peptide sequencing; comparison of spectra for free and tagged peptides allows assignment of fragment ions through mass shifts of c ions. In a series of two articles, Peter Armentrout and Amy Heaton explore the thermodynamics and mechanisms of protonated diglycine decompositions. The first paper presents a full computational description of the fragmentation reactions, while the second paper presents experimental results of CID processes in a guided ion beam tandem mass spectrometer. The contribution from Alan Marshall and co-workers describes studies of the relative stability of peptide sequence ions generated by tandem mass spectrometry;

unimolecular dissociation by infrared radiation allows determination of relative activation energies for fragmentation. Stephen Stein and co-authors investigate the formation of $y+10$ and $y+11$ ions in the collision-induced dissociation of peptide ions; they explore the abundance of these ions for different residues at the N-terminus. In the final paper, Béla Paizs, Benjamin Bythell, and Philippe Maître characterize the rearrangement pathway of the a_4 ion of protonated YGGFL by IR spectroscopy and modeling; their data confirm the presence of a mixture of gas phase structures. This collection of papers clearly shows the vibrancy of the field of peptide fragmentation and our growing understanding of the complexities of these important processes.

The *Journal of the American Society for Mass Spectrometry* is privileged to present this issue to highlight the exceptional accomplishments of Béla Paizs. We look forward to future exciting developments in the characterization of peptide fragmentation reactions and peptide ion structures in the gas phase.

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