# LAKE LOUISE XVI

# 16th Workshop on Tandem Mass Spectrometry

# Thursday, December 4, 2003

# Chair: Gary Glish

- 8:05 Introductory Remarks
- 8:15 Copper-Mediated Radical Cations of Peptides, K.W. Michael Siu, York U.
- 8:55 Controlling fragmentation of peptides for protein identification, Isabel Riba Garcia, Simon Gaskell, UMIST
- 9:15 Peptide Fragmentation as a function of Laser Fluence in a MALDI TOF-TOF, *Alfred Yergey*<sup>1</sup>, Jennifer Campbell<sup>2</sup>, Paul Blank<sup>1</sup>, Marvin Vestal<sup>2</sup>, Stephan Stein<sup>3</sup>, <sup>1</sup>NIH, <sup>2</sup>ABI, <sup>3</sup>NIST
- 9:35 Surface-Induced Dissociation of MALDI Ions in FT-ICR MS, *Julia Laskin*, Kenneth Beck, John Hache, Jean Futrell, PNL

# 9:55 Discussion

# 10:00 Break

- 10:20 Linear Quadrupoles with Added Octopole Fields, Don Douglas, U. of British Columbia
- 10:40 Using Single Analyte Resolved In-Source CID and Accurate Mass Measurement for the Analysis of Peptides and Small Molecules, *John Fjeldsted*, Agilent
- 11:00 Travelling Wave Ion Propulsion in a Collision Cell, *Kevin Giles*, Steve Pringle, Ken Worthington, Bob Bateman, Waters Corp.
- 11:20 ECD and Positive Ion/Negative Ion Reactions in the IonSpec Closed Cylindrical Cell, *Robert T. McIver*, Kevin Crellin, IonSpec Corp.
- 11:40 High Throughput, Data Dependent Analysis using a Hybrid Ion Trap-FTICR Mass Spectrometer, *Lester Taylor*, Thermo Electron Corp.

## 12:00 Discussion

## Chair: Paul Mayer

- 14:00 Protein Folding Mechanisms and Noncovalent Ligand-Protein Interactions Studied by ESI-MS, *Lars Konermann*, Sonya M. Clark, Douglas A. Simmons, Derek J. Wilson, U. of Western Ontario
- 14:40 A Proteomic Approach for Identification of Bacteria Using Tandem Mass Spectrometry, *Jacek P. Dworzanski*, A. Peter Snyder, Rui Chen, Haiyan Zhang, David Wishart, Liang Li, Geo-Centers, Inc./US Army Edgewood Chemical Biological Center
- 15:00 Direct identification of low mass bacterial biomarkers by MALDI MS and MS/MS of whole cells, *V. Ruelle*<sup>1</sup>, P. Verhaert<sup>2</sup>, E. De Pauw<sup>1</sup>, <sup>1</sup>U. of Liège, <sup>2</sup>U. of Leuven and U. of Maastricht

## 15:20 Discussion

#### 15:25 Break

- 15:50 Environmental Mass Spectrometry: Emerging Contaminants and Current Issues, *Susan Richardson*, US EPA
- 16:30 A Tandem Mass Spectrometric Study at High Mass Accuracy of Flavonoid Mono- and Di-glycosides, *Raymond E. March*<sup>1</sup>, Errol G. Lewars<sup>1</sup>, C. Stadey<sup>1</sup>, Xiu-Sheng Miao<sup>1</sup>, Chris D. Metcalfe<sup>1</sup>, Maciej Stobiecki<sup>2</sup>, Lukasz Marczak<sup>2</sup>, <sup>1</sup>Trent U., <sup>2</sup>Polish Academy of Science

- 16:50 Offline HPLC MALDI Tandem Mass Spectrometry for the Quantification of Pharmaceutical Drugs, *Panos Hatsis*, Dietrich A. Volmer, Institute for Marine Biosciences
- 17:10 Even clinicians prefer Tandem MS test results over immunoassays for differential diagnosis of various diseases, *Ravinder J. Singh*, Mayo Clinic

# 17:30 Discussion

Break for dinner

Chair: Gord McKay

20:00 From Milligrams to Femtograms: A Mass Spec Analyst's Experience Through Thirty Years, *Lawrence Hogge* and Colleagues

#### 21:00 Discussion

21:10 Poster Session

# Friday, December 5, 2003

Chair: John Klassen

- 8:30 Folding and Dynamics of Proteins and Protein Complexes Monitored by Mass Spectrometry, *Albert Heck*, Ultrecht U.
- 9:10 Top Down MS/MS Characterization of Disulfide Bonds by Electron Capture Dissociation and IR Multiphoton Dissociation, *Huili Zhai*, Fred McLafferty, Cornell U.
- 9:30 Initiating Analysis of the Proteome of the Ciliated Protozoan Tetrahymena thermophila, *Jeffrey C. Smith*, Kalkidan Belay, Scott Beeser, Alex Keuroghlian, Ronald E. Pearlman, K.W. Michael Siu, York U.
- 9:50 Tissue Proteomics: An Analytical Chemist's Dream (and Nightmare), *Liang Li*, U. Alberta

## 10:10 Discussion

10:15 Break

- 10:35 Towards Quantifying Internal Energy Deposition at keV Collision Energies, Clement Poon, *Paul M. Mayer*, U. of Ottawa
- 10:55 Spin Conservation in the Unimolecular Dissociation of Ionic Complexes between NO and Aromatics, *Julie A.D. Grabowy*, Paul M. Mayer, U. of Ottawa
- 11:15 Comparative Analysis of Peptide Modifications on Quadrapole-Linear Ion Trap and Quadrapole-Time of flight Instruments, *Juergen Kast*, U. of British Columbia
- 11:35 Imaging MALDI with an orthogonal TOF mass spectrometer, *Werner Ens*, Gamini Piyadasa, James McNabb, Victor Spicer, Kenneth G Standing, U. of Manitoba

## 11:55 Discussion

Afternoon Free

19:00 Workshop Banquet

# Saturday, December 6, 2003

Chair: Simon Gaskell

- 8:45 Isotopically Coded Cleavable Crosslinker Combined with Tandem MS for Studying Protein Complexes, *Christoph Borchers*, U. of North Carolina
- 9:05 Structural Characterisation of Outer Cell-Envelope Glycoproteins and their Glycans from Mycobacterium avium, *A.M. Taylor*<sup>1</sup>, A. Gruhl<sup>2</sup>, O. Holst<sup>2</sup>, J.E. Thomas-Oates<sup>1</sup>, <sup>1</sup>U. of York, <sup>2</sup> Borstel Research Centre

- 9:25 A Novel Approach for Mapping O-Linked Glycosylation in Pseudomonas Aeruginosa Through Comparison of Isotope Maps Before and After \(\beta\)-Elimination Followed by Targeted LC/MS/MS, *Michael Schirm*<sup>1</sup>; Susan Logan<sup>2</sup>; I. Schoenhofenf<sup>2</sup>; Karen Waldron<sup>1</sup>; Pierre Thibault<sup>3</sup>, <sup>1</sup>U. of Montreal, <sup>2</sup>Institute for Biological Sciences, <sup>3</sup>Caprion Pharmaceuticals Inc
- 9:45 Discussion
- 9:55 Break
- 10:15 Techniques for Enhanced High-Throughput HPLC/MALDI-MS/MS Analysis of Small Pharmaceutical Drugs, *Dietrich Volmer*, Institute for Marine Biosciences
- 10:35 Determinations of Protein Complex Association Constants with the Titration Method: Constraints Imposed by the ESI Mechanism, Michael Peschke, Udo Verkerk, *Paul Kebarle*, U. Alberta
- 10:55 How much mass accuracy is needed for high throughput proteomics, *Daniel Boismenu*, McGill U.
- 11:15 Direct tissue peptidomics; evolution in the past two years, *Peter Verhaert*, U. of Leuven and U. of Maastricht
- 11:35 IRMPD of Intact Proteins in a Quadrupole Ion Trap, David M. Black, Johanna Stephens, *Gary L. Glish*, U. of North Carolina
- 11:55 Closing Remarks

#### **Posters**

Analysis of cisplatin and its hydrolysis products by ESI-ITMS and high-field asymmetric waveform ion mobility spectrometry, Meng Cui, Luyi Ding and *Zoltán Mester*, Institute for National Measurement Standards, National Research Council Canada

How to not re-sequence a proteome: Peptide MS/MS Libraries, Wade Hines, Beyond Genomics

Comparative Proteomics by Isotopic Coding of Lysine Residues, *Jeremy E. Melanson*, Kenneth A. Chisholm, Steven J. Locke, Devanand M. Pinto, Institute for Marine Biosciences

Approaches to the analysis of 3-chloro-4-(dichloromethyl)-5-hydroxy-2(5H)-furanone (MX): a mass spectrometric study, M.A. Trikoupis, V.Y. Taguchi, Ontario Ministry of the Environment Recent Experiences with a QToF Instrument for the Analysis of Chemical Warfare Agents, *Paul A. D'Agostino*, *Claude L. Chenier*, James R. Hancock, DRDC

Two Dimensional Offline HPLC/MS/MS as a tool to elucidate differences in Protein Expression patterns from patients with a genetic disorder and their healthy relatives, Martin Vollmer<sup>1</sup>, Patric Hörth<sup>1</sup>, Edgar Nägele<sup>1</sup>, *Linda Côté*<sup>1</sup> Friedhelm Hildebrandt<sup>2</sup>, <sup>1</sup>Agilent, <sup>2</sup>U. of Michigan

Laser Desorption, Uv-Resonant Multiphoton Ionization, And Tunable Resonant Photodissociation Of Large Molecules In Ion-Trap MS, Mike Blades, August Specht, Denis Roland, John Hepburn, Ken Wright, U. of British Columbia

Fluorescence Spectroscopy of Molecular Ions in a Paul Trap, *Mike Blades*, Ken Wright, U. of British Columbia

Detection of Phosphorylated Peptides from Data Dependent MS3 Neutral-Loss Scans using a Linear Ion Trap Mass Spectrometer, Amy Zumwalt, Gargi Choudhary, Diane Cho, Eric Hemenway, Iain Mylchreest, Thermo Electron Corp.

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Shotgun Sequencing of the Human Cerebrospinal Fluid Proteome Using 2D Chromatography in Combination with Linear Ion Trap Mass Spectrometry, A.F. Hühmer<sup>1</sup>, R.G. Biringer<sup>1</sup>, H. Amato<sup>1</sup>, M. Harrington<sup>2</sup>, <sup>1</sup>Thermo Electron, <sup>2</sup>Huntington Research Institutes

Quantification of Selected Sulfonylurea Herbicides in Canadian Prairie Wetlands Utilizing Electrospray Ionization Mass Spectrometry and Multiple Reaction Monitoring, John V. Headley, *Kerry M. Peru*, Allan Cessna, Jonathan Bailey, Environment Canada

A Preliminary Comparison of MASCOT, MASCOT Distiller and ProteinLynx Global Server 2.0 for Searching Primary Sequence Databases using Peptide LC-MS/MS Data, *Doug Olson*, Andrew Ross, NRC Saskatoon

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