Dear Friends and Colleagues:

On behalf of the Abstract Committee, let me welcome you to HUPO2009 World Congress and to Toronto. Thanks to your enthusiastic support and contributions, we have put together an excellent and comprehensive program covering a wide-spectrum of proteomic science from 36 countries. This Proceeding Book provides all programmatic information as we have it when we go to press, including the program overview, the over 920 abstracts that you submitted and sorted according to the 33 categories that you had chosen, as well as information on invited speakers and Young Investigator Awardees. We are pleased to be able to put together an oral program that comprises some 150 presentations, most of which are selected from the abstracts that you submitted.

We thank the editorial efforts of Dr. Peipei Ping and her associates, as well as the production teams of Clinical Proteomics for bringing our concept of a Proceeding Book to fruition.

Thank you again for your enthusiastic support. Have a great conference!

Professor K.W. Michael Siu

Chair of Abstract Review Committee

On behalf of HUPO 2009 Organizing Committee

HUPO2009 World Congress Organizing Committee

Christoph Borchers, PhD
Director, Genome BC Proteomics Centre
University of Victoria, Canada

Michael Siu, PhD
Director, Centre for Research in Mass Spectrometry, York University, Canada

David Fenyo, PhD
Senior Research Scientist
The Rockefeller University, USA

Peipei Ping, PhD
Professor and Director
Physiology and Medicine
UCLA School of Medicine, USA

Peter Liu, MD
Scientific Director, ICRH
Professor of Medicine and Physiology at the University of Toronto, Canada

John Yates, PhD
Director, Mass Spectrometry Lab
Department of Chemical Physiology
The Scripps Research Institute, USA
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The Multicultural Canadian Experience Welcomes You at HUPO2009 World Congress.
Introduction:
Extraction of proteins and peptides from body fluids and tissues is a crucial step during sample preparation for proteomic profiling. Body fluids such as serum or plasma are pre-fractionated to break down sample complexity e.g. by liquid chromatography or magnetic beads prior to mass spectrometry. Preparing proteins from tissue or cell culture prior to MALDI-TOF mass spectrometry is a much more demanding step regarding buffer composition and extraction conditions compared to the fractionation of serum or plasma.

Here, we present the development of optimised conditions of protein extraction from rat tissue and cell cultures. Several different extraction buffers and disruption methods were tested in order to obtain MALDI-TOF MS compatible protein solutions. Also, we tested the impact of pre-fractionation with magnetic beads compared to direct deposit onto MALDI targets.

Methods:
Rat tissues and lymphoblastoid cell lines were used to extract proteins and peptides. Buffers containing detergents, salts and chaotropes were tested as well as mechanical disruption with glass beads (Qiagen TissueLyser), with a protein extraction kit (Allprep DNA/RNA/Protein kit, Qiagen) and targeted ultrasound (KBioscience, Covaris). The extracts were tested for protein concentration (BCA assay), for fragment composition (SDS PAGE) and were either applied to magnetic beads for fractionation (Bruker Daltonic) or directly applied to MALDI-TOF MS (Ultraflex II, Bruker Daltonics) after mixing with alpha-Cyano-4-hydroxycinnamic acid.

Results:
We tested several buffer systems on rat liver, fat and muscle. The best buffer composition regarding protein yield and MS peak number consisted of 50 mM Tris-HCl (pH 7.5), 50 mM ammonium phosphate, 1% CHAPS, 7 M urea and 2 M thiourea.

Also, we tested the efficiency of three different protein extraction methods on lymphoblastoid cell lines. The most efficient method was the cell disruption with targeted ultrasound which yielded a 600% higher protein quantity than the protein extraction kit, and 65% more than the mechanical disruption (fig 1).

Furthermore, the extract obtained by the extraction kit was not suitable for MALDI-TOF MS due to the high amount of SDS in the extraction buffer.

Innovative aspects
- Application of targeted ultrasound improves the efficiency of cell disruption
- Ammonium phosphate buffers improve peptide read-out with MALDI-TOF MS
- Fast and reliable protein extraction due to fewer preparations steps