BIOGRAPHICAL SKETCH

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NAME McComb, Mark Errol	POSITION TITLE Assistant Research Professor Director, Cardiovascular Proteomics Center Core Laboratory
eRA COMMONS USER NAME MFMCCOMB	

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	YEAR(s)	FIELD OF STUDY
University of Manitoba	B.S.	1994	Analytical Chemistry
University of Manitoba	M.S.	1996	Analytical Chemistry
University of Manitoba	Ph.D.	2000	Analytical Chemistry
Boston University School of Medicine	Post-doc	2002	Mass Spectrometry

A. Personal Statement

My interests encompass the development and application of mass spectrometry (MS) and proteomics based technologies for the characterization of human disease. The foundation of clinical proteomics dictates that alterations in the abundance of plasma proteins reflect systemic changes associated with disease and thus may serve as biomarkers. Fundamental studies encompass high-throughput sample processing strategies for matrix assisted laser desorption ionization (MALDI) and electrospray (ESI) MS, analytical separation science coupled with MS, instrument development and interface development, advanced large scale data interrogation techniques and robust statistical modeling and validation. Biological and clinical applications through in-house study and collaborative aims focus on protein expression characterization and post-translational modification (PTM) characterization related to the identification and progression of disease states from models and patient studies. Specific emphasis is placed on the characterization of PTMs, specifically protein glycosylation and PTMs induced via oxidative stress (OPTMs). Several disease models are targeted which include elucidation of biomarkers indicative of specific biochemical pathways related to cancer progression as well as those associated with cardio-protective pathways which result as a function of oxidative stress on the host environment.

B. Positions and Honors

Positions and Employment

2010-present Director, Biomarkers Associated research Collaborative, BUSM, Boston, MA.
2006-present Assistant Research Professor, Department of Medicine, BUSM, Boston, MA.
2002-present Director, Core Laboratory, Cardiovascular Proteomics Center, BUSM, Boston, MA
2000-2002 Post-doctoral Fellow, Mass Spectrometry Resource, BUSM, Boston, MA
1993-2000 Teaching Assistant, Chemistry, University of Manitoba, Winnipeg, MB, Canada

Other Experience and Professional Memberships

2010-present National Heart Lung and Blood Institutes Proteomics Initiative
2010-present Editorial board: OMICS – J. Chromatography & Separation Techniques
2007-present Peer Review Panel, National Cancer Institute, Cancer Prevention Research Small Grants
2007-present Peer Review Panel, National Science Foundation NSF SBIR Phase I Grants
2004-2008 Organizing Committee, OPTM in the Cardiovascular System, Boston, MA
2002-2009 National Heart Lung and Blood Institutes Proteomics Initiative

2001-2002 Program Committee, American Society for Mass Spectrometry

2001-present Ad-hoc Review: National Institutes of Health: NCI, NCRR, NHLBI, Canadian Institute of Health Research, National Sciences and Engineering Research Council of Canada

1993-present Memberships: Human Proteome Organization (HUPO, US-HUPO), Association of Biomolecular resource Facilities (ABRF), American Society for Mass Spectrometry (ASMS), American Chemical Society (ACS), Canadian Society for Chemistry (CSC), Canadian Society for Mass Spectrometry (CSMS)

2000-present Select Publications Review: J. Proteome Research, Proteomics, J. Mass Spectrometry, J. American Society for Mass Spectrometry, Analytical Chemistry, Circulation Research, Electrophoresis, Analytical Biochemistry, Molecular Diagnosis and Therapy, Proteomics Clinical Applications, Rapid Communications in Mass Spectrometry, J. Experimental Medicine, J. Proteomics

Honors

2000-2002 National Science and Engineering Research Council of Canada Post-Doctoral Fellowship

1999-2000 Ryan/Harris Award, Chemical Institute of Canada

1996-2000 Graduate Research Fellowship, University of Manitoba, Winnipeg, MB, Canada

1996-2000 Graduate Fellowship, Chemistry, University of Manitoba, Winnipeg, MB, Canada

Patents: McComb, M.E., Oleschuk, R.D., Manley, D.M., Donald, L., O'Neil, J.D.J., Chow, A., Ens, W., Standing, K.G., Perreault, H., 1998, Use of Polyurethane Membrane for MALDI-TOFMS Analysis of Whole Blood, Canadian Patent # 2,228,413. US Patent #073,364.

C. Publications from 2006

1. Cohen, R. A. and **McComb, M.E.**, Preconditioning enters the era of "physiological proteomics". Circ Res, 2006. 99(7): p. 663-665.
2. Dauly, C., Perlman, D. H., Costello, C. E., and **McComb, M.E.**, Protein separation and characterization by np-RP-HPLC followed by intact MALDI-TOF mass spectrometry and peptide mass mapping analyses. Journal of Proteome Research, 2006. 5(7): p. 1688-1700.
3. Denis, G. V., **McComb, M.E.**, Faller, D. V., Sinha, A., Romesser, P. B., and Costello, C. E., Identification of transcription complexes that contain the double bromodomain protein Brd2 and chromatin remodeling machines. Journal of Proteome Research, 2006. 5(3): p. 502-511.
4. **McComb, M.E.**, Perlman, D. H., Huang, H., and Costello, C. E., Evaluation of an on-target sample preparation system for matrix-assisted laser desorption-ionization time-of-flight mass spectrometry in conjunction with normal-flow peptide high-performance liquid chromatography for peptide mass fingerprint analyses. Rapid Communications in Mass Spectrometry, 2007. 21(1): p. 44-58.
5. Odhiambo, A., Perlman, D. H., Huang, H., Costello, C. E., Farber, H. W., Steinberg, M. H., **McComb, M.E.**, and Klings, E. S., Identification of oxidative post-translational modification of serum albumin in patients with idiopathic pulmonary arterial hypertension and pulmonary hypertension of sickle cell anemia. Rapid Communications in Mass Spectrometry, 2007. 21(14): p. 2195-2203.
6. Perlman, D. H., Huang, H., Dauly, C., Costello, C. E., and **McComb, M.E.**, Coupling of protein HPLC to MALDI-TOF MS using an on-target device for fraction collection, concentration, digestion, desalting, and matrix-analyte cocrystallization. Analytical Chemistry, 2007. 79(5): p. 2058-2066.

7. Saba, J. A., **McComb, M.E.**, Potts, D. L., Costello, C. E., and Amar, S., Proteomic mapping of stimulus-specific signaling pathways involved in THP-1 cells exposed to Porphyromonas gingivalis or its purified components. Journal of Proteome Research, 2007. 6(6): p. 2211-2221.
8. Sethuraman, M., Clavreul, N., Huang, H., **McComb, M.E.**, Costello, C. E., and Cohen, R. A., Quantification of oxidative posttranslational modifications of cysteine thiols of p21ras associated with redox modulation of activity using isotope-coded affinity tags and mass spectrometry. Free Radical Biology and Medicine, 2007. 42(6): p. 823-829.
9. Lavatelli, F., Perlman, D. H., Spencer, B., Prokaeva, T., **McComb, M.E.**, Théberge, R., Connors, L. H., Bellotti, V., Seldin, D. C., Merlini, G., Skinner, M., and Costello, C. E., Amyloidogenic and associated proteins in systemic amyloidosis proteome of adipose tissue. Molecular & Cellular Proteomics, 2008. 7(8): p. 1570-1583.
10. Mathivanan, S., Ahmed, M., ..., **McComb, M.E.**, ..., and Pandey, A., Human Proteinpedia enables sharing of human protein data. Nature Biotechnology, 2008. 26(2): p. 164-167.
11. Bhatia, V. N., Perlman, D. H., Costello, C. E., and **McComb, M.E.**, Software Tool for Researching Annotations of Proteins: Open-Source Protein Annotation Software with Data Visualization. Analytical Chemistry, 2009. 81(23): p. 9819-9823.
12. Perlman, D. H., Bauer, S. M., Ashrafian, H., Bryan, N. S., Garcia-Saura, M. F., Lim, C. C., Fernandez, B. O., Infusini, G., **McComb, M.E.**, Costello, C. E., and Feelisch, M., Mechanistic Insights Into Nitrite-Induced Cardioprotection Using an Integrated Metabolomic-Proteomic Approach. Circulation Research, 2009. 104(6): p. 796-U170.
13. Rex, S., Beaulieu, L. M., Perlman, D. H., Vitseva, O., Blair, P. S., **McComb, M.E.**, Costello, C. E., and Freedman, J. E., Immune versus thrombotic stimulation of platelets differentially regulates signalling pathways, intracellular protein-protein interactions, and alpha-granule release. Thrombosis and Haemostasis, 2009. 102(1): p. 97-110.
14. Romesser, P. B., Perlman, D. H., Faller, D. V., Costello, C. E., **McComb, M.E.**, and Denis, G. V., Development of a Malignancy-Associated Proteomic Signature for Diffuse Large B-Cell Lymphoma. American Journal of Pathology, 2009. 175(1): p. 25-35.
15. Ying, W. T., Perlman, D. H., Li, L., Théberge, R., Costello, C. E., and **McComb, M.E.**, Highly efficient and selective enrichment of peptide subsets combining fluorous chemistry with reversed-phase chromatography. Rapid Communications in Mass Spectrometry, 2009. 23(24): p. 4019-4030.
16. Zee, R.S., Yoo, C.B., Pimentel, D.R., Perlman, D.H., Burgoyne, J.R., Hou, X., **McComb, M.E.**, Costello, C.E., Cohen, R.A., Bachschmid, M.M., Redox regulation of sirtuin-1 is mediated by Sglutathiolation, Antioxidants & Redox Signaling, 2010. 13(7): p. 1023-1032.
17. Théberge, R. Infusini, G., Tong, W., **McComb, M.E.**, Costello, C.E., Top-down analysis of small plasma proteins using an LTQ-Orbitrap: Potential for mass spectrometry-based clinical assays for transthyretin and haemoglobin, Int. J. Mass Spectrom., 2011. 300(2-3): p. 130-142.
18. Chen V.C., Sadler, G., **McComb, M.E.**, Perreault, H., Duckworth, H.W., Characterization of Specific Binding by Mass Spectrometry: Associations of E. Coli Citrate Synthase with NADH and 2-AzidoATP, Int. J. Mass Spectrom., 2011. 305: p. 238-246.

D. Research Support

<u>Ongoing Research Support</u>:

N01-HV-10-05_(2) Director, Core Laboratory, Costello, C.E. (PI) 08/15/10-7/31/15
NIH-NHLBI

Modification of Cardiovascular Proteins by Metabolic Disease
Investigate protein and post-translational expression changes that arise due to pathology of metabolic disease in patient populations. Targeted program to develop biomarker signatures of metabolic disease.

No Number Co-PI; Goldberg, B. (PI) 07/01/10-06/30/11
Photonics Center FTDA Program, BU
Quantified high-throughput biomarker discovery by mass spectrometry on label-free arrays
Develop array based technology for biomarker measurement using Spectral Reflectance Biosensing and MS

No Number Director, PI 05/01/10-04/30/11
Evans Center ARC Program, BUSM
Biomarkers Associated Research Collaborative
Investigate biomarkers in pilot projects of cardiovascular disease.

Completed
N01-HV-28178 Core Laboratory Director, Costello, C.E. (PI) 10/01/02-9/30/09
(extended 04/30/2010)
NIH-NHLBI
Oxidative Post-Translational Modifications of Cardiovascular Disease
Investigate post-translational modifications that may be important in the signaling mechanisms of proteins that are altered by oxidative chemical reactions in cardiovascular disease.

2R01 HL68970-06 Co-Investigator, Steinberg, M.H. (PI) 8/01/06-7/01/10
NIH-NHLBI
Genetic Modulation of Sickle Cell Anemia
Aim 3: PROTEIN MODIFICATION IN SICKLE PLASMA: 1- Identify protein bio-markers and protein post-translational modification markers for sickle cell disease induced pulmonary hypertension.

S10 RR 025082 Co-Investigator, Costello, C.E. (PI) 01/01/09-12/31/09
NIH/NCRR
LTQ-FT MS System for On-line Protein and Glycan Analysis
This system will enable the identification of proteins and their post-translational modifications, glycoconjugates and free glycans, to determine structure/activity relationships and variations as a function of development and disease.

P41-RR-10888 Research Associate, Costello, C.E. (PI) 4/01/01-3/31/06
NIH-NCRR
Mass Spectrometry Resource
The goals of the resource are to advance mass spectrometric methods and instrumentation to meet the needs of biochemistry and medicine, identify new areas appropriate for mass spectrometry in the health sciences and to develop new approaches using this technology, apply cutting edge mass spectrometry to solve critical questions in the life sciences, train students, postdoctoral fellows and practicing scientists in mass spectrometry, and educate the community about modern mass spectrometry and to encourage its wide and appropriate use.