BIOGRAPHICAL SKETCH

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NAME: Lam, Ying-Wai

eRA COMMONS USER NAME (credential, e.g., agency login): LAMYING

POSITION TITLE: Director of VBRN Proteomics Facility, Research Associate Professor of Biology

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
The Chinese University of Hong Kong, Hong Kong	B.Sc.	12/1998	Biochemistry
The Chinese University of Hong Kong, Hong Kong	Ph.D.	12/2001	Protein Biochemistry
University of Massachusetts Medical School, US	Postdoctoral	09/2005	Cancer Proteomics

A. Personal Statement

I direct the Vermont Biomedical Research Network (VBRN, formally Vermont Genetics Network (VGN)) Proteomics Facility at the University of Vermont (supported by P20GM103449) with the goals of providing expertise and the state-of-the-art proteomics technology to researchers, as well as establishing an educational environment for sharing experience and knowledge in proteomics. I have extensive experience in applying mass spectrometry-based proteomics strategies to solve a variety of biological questions. Since joining UVM/VGN as director of the Proteomics Facility in 2011, I have worked directly with **66** UVM faculty, **16** staff, **15** postdocs, and **37** graduate students, as well as **29** external investigators providing guidance and support for their proteomics projects from initial experimental design, sample preparation, and instrument operation, to data analysis and interpretation. Since 2012, I have co-authored **30** publications with UVM investigators and external users on a variety of projects interfacing biology, biochemistry, and proteomics. Together with my facility colleagues, we maintain the operation of facility instrumentation (LTQ linear ion trap MS, LTQ-XL-ETD linear ion trap MS, LTQ-Orbitrap Discovery MS, Exploris 240 MS, and Orbitrap Eclipse Tribrid MS), evaluate new technologies and software, as well as develop methodologies to address emerging proteomics and mass spectrometry needs. I give seminars, guest lectures and facility tours to faculty, faculty candidates, undergraduate and graduate students from UVM, Primarily Undergraduate Institutions, and other institutions. I am a research advisor or collaborator for 7 faculty members from our Baccalaureate Partner Institutions on proteomics and mass spectrometry.

Besides initiating proteomics projects and publishing results, I have also assisted investigators in obtaining intramural and extramural funding. Since 2012, I have provided 97 letters of support as collaborator, key personnel, other significant contributor, or consultant for grant applications (new or renewal) to federal and non-federal agencies. **Twenty-three** have been funded, **6** are currently active (underlined) (**13 from NIH**: F32HL129706 (Heppner), R01DE014711 (Spatafora), R15GM123393 (Hass), R01HL122383 (Anathy), R01NS045940 (Cipolla), R01AI105191(Ward), R01HL085646 (Van der Vliet), R01HL138708 (Van der Vliet), R01HL137268 (van der Vliet/Dixon), R01GM054899 (Francklyn), R01GM117155 (Jordan, Johns Hopkins Univ.), F31HL142221 (Dustin), R56AG074488 (Janssen-Heininger); **1 from DOD**: IDeA W81XWH-14-1-0199 (Shukla); **2 from Foundation**: Hearing Health Foundation Res. Grant (Bond), Preeclampsia Foundation (Ko); **1 from NSF**: MCB 1817793 (Garcia, Castleton Univ.); **1** Hatch Award, USDA-NIFA HATCH VT-H02009 (Greenwood); **3 from UVM**: CVRI ECAC award (Ko), FAHC Res. Award (Krag), COBRE PIP (Dixon); **3 VGN Pilot/Project Award**: (Lamos, Wuorinen, Garcia)).

Ongoing and recently completed NIH grants supporting the proteomics facility that I would like to highlight include:

P20GM103449
Francklyn (PI) Role: Core Facility Director
6/1/20 – 5/31/25
Vermont Genetics Network – Vermont INBRE

P20GM103449
Van Houten / Forehand (PI) Role: Core Facility Director
6/1/15 – 5/31/20
Vermont Genetics Network – Vermont INBRE

Citations:

1. Smith K, Fields J, Voogt R, Deng B, Lam YW and Mintz K: Alteration in abundance of specific membrane proteins of *Aggregatibacter actinomycetemcomitans* is attributed to deletion of the inner membrane protein MorC. ***Proteomics*** 15:1859-67. **2015** PMCID: PMC4456248
2. Tacoma R, Fields J, Ebenstein DB, Lam YW and Greenwood SL: Characterization of the bovine milk proteome in early-lactation Holstein and Jersey breeds of dairy cows. ***Journal of Proteomics*** 130:200-10. **2016** PMCID: PMC4859431
3. Munson P, Lam YW, Dragon J, Macpherson M and Shukla A: Exosomes from asbestos exposed cells modulate gene expression in mesothelial cells. ***FASEB Journal*** 32:4328-4342. **2018** PMCID: PMC6044058
4. Hasan M, Teixeira JE, Lam YW, Huston CD: Coactosin phosphorylation *controls Entamoeba histolytica* 1 cell membrane protusions and cell motility. ***MBio.*** 11(4):e00660-20 **2020** PMCID: PMC7407079

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2020-Present Director, Vermont Biomedical Research Network Proteomics Facility
2019-Present Research Associate Professor, Department of Biology, University of Vermont, Vermont
2019-Present Member, Association of Biomolecular Resource Facilities
2014-Present Faculty, Graduate College, University of Vermont
2011-Present Director, Vermont Genetics Network Proteomics Facility
2011-2019 Research Assistant Professor, Department of Biology, University of Vermont, Vermont
2009-2011 Mentor on Gene-Environment Interactions Training Program (GEITP), NIEHS, T32ES016646
2005-2011 Research Assistant Professor, Department of Environmental Health, Division of Environmental Genetics and Molecular Toxicology, University of Cincinnati College of Medicine, Cincinnati, OH
2002-Present Member, American Society for Mass Spectrometry
2002-Present Member, American Chemical Society

Honors

2003-2005 Department of Defense - Prostate Cancer Program Postdoctoral Research Award "Proteomics Approach to Evaluate the Impact of Diet and Stress Reduction on Prostate Cancer Progression", Role: PI - $98,000
Aug. 2005 Partial Travel Award, American Urological Association/ Society for Basic Urologic Research Summer Research Conference, "Inflammation in Prostate Diseases"

C. Contributions to Science

1. Research collaborations - applying proteomics to a wide range of research areas

I have collaborated with many investigators and applied an array of state-of-the-art mass spectrometry-based proteomics strategies to their studies, ranging from routine protein identification, protein interaction

and post-translational modification characterization (e.g., acetylation, methylation, phosphorylation, glutathionylation, etc.), to large-scale quantitative proteomic analyses using stable isotopes (stable isotope labeling by amino acids in cell culture, dimethyl labeling, and tandem mass tags (TMT)). Some of these collaborative efforts involved the use of large-scale proteomics as a discovery platform to generate new hypotheses to address important research questions, which cannot be interrogated by other biochemical or genomics strategies.

I co-designed and helped develop in-house workflows and guided graduate students to establish methods specific to their research projects, for example, dimethyl labeling and strong cation exchange separation workflow for elucidating *A. actinomycetemcomitans* membrane proteome (Smith et al., *Proteomics*, 2015), and enrichment workflows for stable isotope-based phosphoproteomics in *Entamoeba histolytica* (Hasan et al., *MBio*. 2020). I also established specific mass spectrometry experiments with investigators for their specialized projects, for example, mapping novel cleavage sites (Lee et al., *Molecular Neurodegeneration*, 2017), identification and quantification of phosphorylation and *S*-sulfenylation using stable isotopes and parallel reaction monitoring (PRM) (Krishnamurthy et al., *MBio*, 2016; Heppner et al, *Nature Communications*, 2018), and elucidating exosome protein content under asbestos exposure using gel-based fractionation method and TMT labeling (Munson et al., *FASEB J*, 2018. The results were published in the journals of investigators' interest with proteomics as a main focus or in leading proteomics journals (e.g., *Journal of Proteomics*, *Proteomics*).

a. Krishnamurthy S, Deng B, del Rio R, Urban S, Boothroy J, Lam YW and Ward GE: Not a simple tether: Binding of *Toxoplasma gondii* AMA1 to RON2 during invasion protects AMA1 from rhomboid-mediated cleavage and leads to dephosphorylation of its cytosolic tail. ***MBio*** 7 pii: e00754-16. ***2*016** PMCID: PMC5021801
b. Lee CW, Stankowski JN, Chew J, Cook C, Lam YW, Almeida S, Carlomagno Y, Lau KF, Prudencio M, Gao FB, Bogyo M, Dickson DW and Petrucelli L: The lysosomal protein cathepsin L is a progranulin protease. ***Molecular Neurodegeneration*** 12:55. **2017** PMCID: PMC5526245
c. Heppner DE, Dustin CM, Liao C, Hristova M, Veith C, Little AC, Ahlers BA, White SL, Deng B, Lam YW, Li J and van der Vliet A: Direct Cysteine Sulfenylation Drives Src Kinase Activation. ***Nature Communications*** 9:4522. **2018** PMCID: PMC6207713
d. Kumar A, Elko E, Bruno SR, Mark ZF, Chamberlain N, Korwin-Mihavics B, Chandrasekaran R, Walzer J, Ruban M, Gold C, Lam YW, Ghandikotad S, Jeggad AG, Gomez JL, Janssen-Heininger YMW and Anathy V: Inhibition of PDIA3 in Club Cells Attenuates Osteopontin Production and Lung Fibrosis. ***Thorax*** 77:669-678 **2021** PMCID: PMC8847543

2. Prostate aging and cancer proteomics
(Postdoctoral research)

My research conducted prior to my current appointment involved the use of proteomics techniques, time-of-flight mass profiling, and stable isotope tagging in conjunction with shotgun sequencing and post-translational modified-site mapping techniques, to identify prostate cancer biomarkers, elucidate the molecular mechanisms of aging and carcinogenesis, as well as to determine the impact of *nitrosative stress-induced protein modifications* (e.g. *S*-nitrosylation on cysteines) and *phosphorylation* on signaling pathways. The results yielded insights into designing and interpreting subsequent hypothesis-driven molecular biology experiments to address the roles of these post-translational modifications in prostate cancer cell migration/invasion (Isaac et al., *Biochemistry*, 51: 9689-9697. 2012).

a. Lam YW, Mobley JA, Evans JE and Ho SM: Mass profiling-directed isolation and identification of a stage-specific serologic protein biomarker of advanced prostate cancer. ***Proteomics*** 5:2927-2938. **2005**
b. Lam YW, Tam NN, Green KM, Evans JE, Zhang X and Ho SM: Differential proteomics in the aging Noble rat ventral prostate. ***Proteomics*** 8:2750-2763. **2008**
c. Lam YW, Yuan Y, Isaac J, Babu CV, Meller J and Ho SM: Comprehensive identification and modified-site mapping of *S*-nitrosylated targets in prostate epithelial cells. ***PLOS ONE*** 5:e9075. **2010** PMCID: PMC2816712

d. Lam HM, Suresh Babu CV, Wang J, Yuan Y, Lam YW, Ho SM and Leung YK: Phosphorylation of human estrogen receptor-beta at serine 105 inhibits cancer cell migration and invasion. ***Molecular and Cellular Endocrinology*** 358:27-35. **2012** PMCID: PMC3348253

3. Small molecule characterization and quantification

I was involved in several projects in collaboration with Dr. Jagjit Yadav and his colleagues at the University of Cincinnati, providing expertise to unambiguously identify and characterize the hydroxy-metabolites of aromatic hydrocarbons using LC-ESI-high resolution mass spectrometry with accurate mass measurements and tandem mass spectrometry. These experiments were critical to the understanding of how the newly identified fungal P450s metabolize environmental toxicants (Syed et al., 2010, 2011, and 2013). At UVM, I applied stable-isotope dilution LC/MS techniques and Selected Reaction Monitoring (SRM) to quantify estradiols in brain tissues (Cherian, Wai Lam et al., *Neuroscience* 2014), with the results supporting the notion that estradiols are locally synthesized in the vomeronasal organs and directly regulate chemoreception.

I also helped chemistry faculty to perform accurate mass measurements to authenticate their compounds of interest in order to fulfill publication requirements of chemistry journals (14 publications, from 2012-2014, citing our grant number in the acknowledgement section).

a. Syed K, Doddapaneni H, Subramanian V, Lam YW and Yadav J: Genome-to-function characterization of P450 monooxygenases oxidizing polycyclic aromatic hydrocarbons (PAHs) in model white rot fungus. ***Biochemical and Biophysical Research Communications*** 399: 492-7. **2010** PMCID: PMC2943217
b. Syed K, Porollo A, Lam YW and Yadav JS: A fungal P450 (CYP5136A3) Capable of oxidizing polycyclic aromatic hydrocarbons and endocrine disrupting alkylphenols: role of Trp(129) and Leu(324). ***PLOS ONE*** 6:e28286. **2011** PMCID: PMC3229547
c. Syed K, Porollo A, Lam YW, Grimmett P and Yadav J: A Catalytically versatile fungal P450 monooxygenase (CYP63A2) capable of oxidizing higher polycyclic aromatic hydrocarbons, alkylphenols and alkanes. ***Applied and Environmental Microbiology*** 79: 2692-702. **2013** PMCID: PMC3623170
d. Cherian S, Wai Lam Y, McDaniels I, Struziak M and Delay R: Estradiol rapidly modulates odor responses in mouse vomeronasal sensory neurons. ***Neuroscience*** 269:43-58. **2014** PMCID: PMC4270699

4. Purification and characterization of defense proteins from various biological sources (graduate research)

My graduate studies focused on chromatographic isolation of new plant and animal defense proteins (lectins, antifungal proteins, and ribosome-inactivating proteins), which play important roles in host defense against exogenous attacks/infections. Subsequent biochemical characterizations yielded insights into the functional roles of these important classes of proteins.

a. Lam YW, Wang HX and Ng TB: A Robust cysteine-deficient chitinase-like antifungal protein from inner shoots of the edible chive *Allium tuberosum.* ***Biochemical and Biophysical Research Communications*** 279: 74-80. **2000**
b. Lam YW, Ng TB and Wang HX: Antiproliferative and antimitogenic activities in a peptide from puffball mushroom *Calvatia caelata.* ***Biochemical and Biophysical Research Communications*** 289: 744-749. **2001**
c. Lam YW and Ng TB: A monomeric mannose-binding lectin from inner shoots of the edible chive (*Allium tuberosum*). ***Journal of Protein Chemistry*** 20: 361-366. **2001**
d. Lam YW and Ng TB: Purification and characterization of a rhamnose-binding lectin from grass carp ovary. ***Protein Expression and Purification*** 26: 378-385. **2002**

Complete List of Published Work in MyBibliography:
(Coauthored 52 peer-reviewed publications)
https://www.ncbi.nlm.nih.gov/myncbi/ying%20wai.lam.1/bibliography/public/