BIOGRAPHICAL SKETCH

NAME: Quijada, Jeniffer

eRA COMMONS USER NAME: jquijada

POSITION TITLE: Postdoctoral Fellow

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE	Completion Date	FIELD OF STUDY
Universidad Simon Bolivar. Caracas, Venezuela	B.S.	05/2004	Chemistry
Northeastern University. Boston, MA.	Ph.D.	05/2017	Chemistry and Chemical Biology
Stanford University. Palo Alto, CA	Postdoctoral	08/2017-Present	Personalized medicine

A. Personal Statement

I have developed a career in science that allow me to have the expertise, leadership, training, soft skills and motivation necessary to execute the proposed research project. In my academic and research training, I have learnt about multidisciplinary science background from chemistry, physics, biochemistry and analytical techniques using specialized instrumentation, as UV-VIS spectrophotometry, infrared, nuclear magnetic resonant, calcium-mobilization assay and mass spectrometry in proteomics analysis. In my PhD project, I successful designed a new and cheaper platform for relative quantitation of intact protein analysis using mass spectrometry using stable isotope labeling. This new platform was demonstrated using prokaryote and eukaryote organism such as *Escherichia coli* (bacteria), *Saccharomyces Cerevisiae* (yeast) and *Drosophila Melanogaster* (fruit flies). This demonstration supports its use of simple and complex organism. Also, the application of low toxicity concentrations of stable isotope labels makes this method a feasible application to mouse model.

Quijada JV, Schmitt ND, Salisbury JP, Auclair JR, Agar JN. Heavy Sugar and Heavy Water Create Tunable Intact Protein Mass Increases for Quantitative MS in any Feed and Organism. Anal. Chem. (2016), 88 (22), pp 11139–11146.

My second PhD research project was on developing a method for measuring protein half-lives using stable isotope labeling on complex organism, *Drosophila Melanogaster* (fruit flies). This information helps to understand the biological pathway and balance of biogenesis, trafficking and degradation of the proteins. The maintenance of a good balance of protein conditions (ex. half-lives) can help in the understanding of disease related with degradation and loss-of-function phenotypes. A healthy protein half-lives is important for a successful organism development, healthy aging, resistant to environmental stress and pathogens. This project won a competitive travel award to be presented in Human Proteome Organization conference (US-HUPO 2017).

Currently, I am a postdoc at Stanford University at Dr. Michael Snyder group, and here I would like to lead my training toward human health study. In our research group, we have been focused on integrating different types of multi-omics analysis, genomics, transcriptomics, proteomics and metabolomic, in the understanding of personalized human health. My contribution to this project will be the acquisition high-throughput data and data analysis using mass spectrometry technique for analysis on proteomics, metabolomics and lipidomics. From my research group, these data will be combined with genomics, transcriptomics and wearable technology for the determination of biomolecules and tracking measurements associated with human variation and health state. In my long-term goals in this project are to translate our finding to a clinical and personalize medicine routine environment that make it easy for people to monitor and improve his/her own health condition. For my long-term goal training, I would like to focus my career on personalized human medicine research and become a leader in this field.

B. Positions and Honors

Positions and Employment

2006-2007 Research Assistant, Department of Biochemistry, The City College of New York, New York, NY
2007-2011 Associate Researcher II, Department of Neuroscience, Mount Sinai School of Medicine, NY
2011-2017 PhD Candidate, Department of Chemistry, Northeastern University. Boston, MA
2017-Present Postdoc, Department of Genetics, Stanford University. Stanford, CA

Other Experience and Professional Memberships

2011-Present Member, American Chemistry Society (ACS)
2012-Present Member, Great Boston Mass Spectrometry Discussion Group (GBMSDG)
2014-Present Member, America Society for Mass Spectrometry (ASMS)
2014-Present Member, Human Proteome Organization (HUPO)

Honors

2013 Award for Protein Purification and Characterization course, Cold Spring Harbor Laboratory Scholarship. Cold Spring Harbor, NY.
2015 Award for Protein Proteomic course, Cold Spring Harbor Laboratory Scholarship. Cold Spring Harbor, NY.
2015 Travel Award for ASMS Conference from the Greater Boston Mass Spectrometry Discussion Group. Boston, MA.
2016 Scientist Mentoring & Diversity Program (SMDP) Biotech Scholar 2016. San Francisco, CA.
2017 US-HUPO Travel Award, Precision Proteomics for Discovery and Health. San Diego, CA.

C. Contributions to Science

1. **Determination of pKa values of unfolded state of proteins measure by Nuclear Magnetic Resonance (NMR)**. Most of study in protein structure has been focused on the folded state, and the information in unfolded state is limited. One of the problem of the unfolded state is the tendency of protein aggregation. This work was focused on the determination of pKa values for unfolded protein using NMR techniques using a denaturant for avoiding protein aggregation. It was demonstrated that the addition of denaturant produces the expected upshift in the pKa values of Glutamic Acid (Glu), but this increasing value is not linear with the concentration of the denaturant. This effect possible shows the complexity of interactions among Glu residue, neighbors residues and with the solvent. My role in this study was to purify the protein, measured protein concentration, set up the NMR experiment, analyzed data and prepared figures for publication.
    a. Quijada J., Lopez G., Versace R., Ramirez L., Tasayco M. On the NMR analysis of pKa values in the unfolded state of proteins by extrapolation to zero denaturant. Biophysical Chemistry, (2007) 129(2-3): 242-250.

2. **Characterization of human sweet taste receptor, a G protein-coupled receptor (GPCR)**. A broad panel of chemically diverse compounds are sweet tasting, including natural sugar, artificial sweeteners and proteins. The binding site of sweet taste compound and the receptor activation is not completed understood. I had worked in collaboration with a research team for the determination of the binding site of the human sweet-taste receptor with different sweet compound activation. In this study, it was characterized the human sweet receptor with the small molecule aspartame and the protein brazzein. In both cases were determined the binding pocket and the amino acids residues that interact with the sweet compound. My role in this study was to design and preparer DNA mutant for the sweet receptor swapping sequences between mouse, monkey and human. I transfected human cells (HEK293) with those DNA mutants, I tested the receptor activation by calcium mobilization assay, I analyzed the data and prepared the plot used for publication. The results of this research are included in three different publications.
    a. Assadi-Porter F., Maillet E., Radek J., **Quijada J**., Markley J., and Max M. Key amino acid residues involved in multi-point binding interactions between brazzein, a sweet protein, and the T1R2–T1R3 human sweet receptor. Mol. Biol. (2010) 398(4): 584-99.
    b. Dittli S., Rao H., Tonelli M., **Quijada J**., Markley J., Max M., and Assadi-Porter F. Structural role of the terminal disulfide bond in the sweetness of brazzein. Chem. Senses (2011) 36 (9): 821-830.

c. Maillet E., Cui M., Jiang P., Mezei M., Hecht E., **Quijada J.**, Margolskee R., Osman R., and Max M. Characterization of the binding site of aspartame in the human sweet taste receptor. Chem. Senses (2015) 40 (8): 577-86.

3. **Develop a fast method for neuropeptide detection using Matrix-Assisted Laser Desorption/Ionization Time-of-flight mass spectrometry (MALDI-TOF MS)**. Traditionally, neuropeptides analysis was performed by Edman sequencing, however this method is slow and does not work with modified neuropeptide in N-terminal. Immunological techniques have been used for neuropeptide quantification, but it is not specifically reliable for single peptide form. In contrast with these previous method, mass spectrometry can detect and identify the precise form of unknown neuropeptides. I participated in the method development of a rapid workflow for detection of neuropeptides using MALDI-TOF MS on *Drosophila melanogaster* brains (fruit flies). My contribution in this study was to take care the fruit flies, made the dissection of the flies adult's brain, prepared sample for MALDI-TOF MS analysis, and acquired the MS spectra.
   a. Salisbury J., Boggio K., Hsu Y., **Quijada J**., Sivachenko A., Gloeckner G., Kowalski P., Easterling M., Rosbash M., Agar J. A rapid MALDI-TOF mass spectrometry workflow for Drosophila melanogaster differential neuropeptidomics. Mol Brain. (2013) 6 (1): 3-32.

D. Additional Information: Scholastic Performance

PhD Program courses and grades: Northeastern University

Courses title	Grade	Courses title	Grade
Analytical Separations	A	Analytical Biochemistry	A-
Principles of Mass Spectrometry	A	Research Skills/Ethics in Chemistry	A-
Optical Methods of Analysis	A	Advanced Laboratory Methods	A
Protein Chemistry	A	Advanced Problem Solving	A
Foundations of Spectroscopy	A		