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Editorial

In the past decade there has been increasing use of proteomics technology in Mexican research and the field of proteomics is now flourishing, in part aided by strong international collaborations and a group of committed and enthusiastic scientists with the vision to bring together the researchers working in the field from all disciplines. This was driven by the founding of the Mexican Proteomics Society or Sociedad Mexicana de Proteomica (SMP). The Society was founded in 2005 by a group of Mexican Researchers led by Drs. Cesar Ferreira Batista and Sergio Encarnacion-Guevara, working in the area of Proteomics with the aim to strengthen and promote the field in this country and to build a community among emerging national proteomics laboratories for the exchange of services, ideas and the training of students; bringing together a multi-disciplinary membership from groups working on human disease to those engaged in applying the technology to issues in plant biology. The initial goal of the Societies executive committee was to organize the 1st Mexican Symposium of Mass Spectrometry — Cellular and Molecular Proteomics, in parallel with a short theoretical course on the Basics of Mass Spectroscopy Applied to Proteomics. These events took place at the Hacienda Cocoyoc in Morelos, from the 19th to the 22nd of October in 2005. More than ten international scientists at the forefront in proteomics were invited to present their work at the meeting, along with speakers from Industry and national scientists who work in the field of proteomics to help stimulate collaborations and provide momentum.

From this exciting start the Society has gone on to have 4 more successful bi-annual meetings. The last of these and the basis for this special issue, was held in Cancun in August of 2013 and was organized by the Executive committee of the Society, at the time led by the president Dr. Victoria Pando Robles. The organizing committee was able to attract an outstanding group of 16 speakers for 5 scientific sessions with the plenary lecture given by Dr. Benjamin Garcia, the Presidential Associate Professor of Biochemistry and Biophysics at the University of Pennsylvania Perelman School of Medicine. Other notable International invited speakers included: Dr. Catherine Costello, Immediate Past-President of HUPO and Professor of Biochemistry, Biophysics and Chemistry at Boston University; Dr. Al Burlingame, Professor of Chemistry and Pharmaceutical Chemistry at UCSF and Co-editor of Molecular and Cellular Proteomics; Dr. Juan J. Calvete, Research Professor of the Spanish Research Council and Editor-in-chief of the Journal of Proteomics; Dr. Marcos

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Eberlin, Professor of Chemistry at the University of Campinas, Brazil and President of the International Mass Spectrometry Society; Dr. Laura Beretta, Professor of Molecular and Cellular Oncology at MD Anderson Cancer Centre, Houston; Dr. Donald Hunt, Professor of Chemistry and Pathology at the University of Virginia; Dr. Hanno Langen, Global Head of Proteomics, Hoffmann-La Roche, and Professor at the University of Basel; Dr. Matthias Selbach, Associate Professor at the Berlin Medical School; Dr. Gary Siuzdak, Professor of Chemistry and Molecular Biology and Director of the Scripps Center for Metabolomics; Dr. Luis Mendoza of the Institute for Systems Biology in Seattle and Dr. Emer Ferro, Professor of Biomedical Sciences at the University of Sao Paulo. National invited speakers included Dr. Sergio Encarnación Guevara, Professor at the Center of Genomic Sciences, UNAM; Dr. Bronwyn Barkla, at the time Associate Professor at the Biotechnology Institute, UNAM; Dr. César Batista, Head of the National Proteomics Laboratory, UNAM; Dr. César López Camarillo, Professor Researcher of the Genomic Sciences Program, UACM; and Dr. Robert Winkler Principal Investigator of the Laboratory of Biochemical and Instrumental Analysis, CINVESTAV Irapuato. The meeting attracted 145 participants representing 15 countries with 50 people also attending the pre-symposium course.

The meeting was supported by the International Centre for Genetic Engineering and Biotechnology as well as the United Nations University Biotechnology program for Latin America and the Caribbean (UNU-BIOLAC) and from the companies Thermo Scientific, Agilent Technologies, Bruker, Bio-Rad, Waters and AccesoLab. From this money 30 students received support to attend both the course and meeting. The majority of scholars were from Mexico, but students from Peru, Colombia, Argentina, Cuba, Brazil, China, India and Egypt were also supported. Overall the meeting was a resounding success made additionally enjoyable by the amazing location and excellent meeting and hotel facilities.

In this Special Issue SMP Cancun 2013 we have brought together some of the outstanding contributions of work that was presented by attendees at this meeting in the form of review articles and original research articles.

I. Proteomics of neglected tropical diseases

Neglected tropical diseases (NTDs) are a medically diverse group of infections caused by different pathogens such as viruses, bacteria, protozoa and helminths. The people who are most affected by these diseases are often the poorest populations, living in remote rural areas and marginal urban areas with poor housing conditions and poor sanitation. The 17 neglected tropical diseases prioritized by the World Health Organizations (WHO) affect more than 1 billion people worldwide and are endemic in 149 countries, including Mexico. In the Mexican research community there are many groups that study pathogens associated with NTDs, however few of them using a proteomics approach. During the Cancun symposium 20 abstracts were presented on NTD's and in this special issue we have 8 contributions; 7 original research articles and one review article.

Dengue is an important global health problem and is the most disseminated NTD. Despite the efforts of the Mexican state to contain and diminish the impact of epidemics, Mexico is fourth on the list of highly dengue endemic countries (WHO). Two articles in this Special Issue are focused on increasing the knowledge about dengue virus (DV) infection. A review article from Salazar et al., 2014, shows the current knowledge about the cellular proteins involved during DV infection in different target cells in the two hosts, mosquito and human. Interestingly DV has a widespread tropism and several proteins have been identified in different cell systems; but extrapolation of these data may not be straight forward since the cross talk between virus and cell proteins may be cell type specific. In this sense, Pando et al., 2014 using label free LC/MS described for the first time the hepatocyte proteome during dengue infection. Results identified 155 differentially expressed proteins and revealed an important decrease in the expression of enzymes involved in the glycolytic pathway, citrate cycle, and pyruvate metabolism; suggesting that mitochondria function could be important during infection. Another pathogen associated with NTDS is *Entamoeba histolytica*, the protozoan parasite responsible for amoebiasis. Four articles in this Special Issue illustrate different aspects of the investigation into this water borne illness. In an outstanding paper, Valdés J., et al., reported for the first time the proteomic isolation of spliceosome complexes in the early-branched eukaryote *E. histolytica*. The genome of this parasite contains nearly 3000 introns and bioinformatic predictions indicate that major and minor spliceosomes occur in Entamoeba. Using tandem mass spectrometry (MS/MS) analyses they identified proteins corresponding to 32 cognate splicing-specific factors, including 13 DExH/D helicases required for all stages of splicing, and 12 different splicing-related helicases were identified also. Furthermore 50 additional proteins involved in co-transcriptional processes were also identified revealing the complexity of co-transcriptional splicing in Entamoeba. On the other hand, De la Cruz, et al., 2014, illustrate that *E. histolytica* EhPC4 transcription factor induces changes in the proteome of the parasite, specifically in actin cytoskeleton proteins, promoting a significant increase in trophozoites motility and destruction of human intestinal cells, a phenomenon associated with virulence. Also they provide experimental evidence about the prominent role of EhABP16 in trophozoites migration. The group of Lopez-Rosas et al., provides experimental evidence for the functional deadenylase activity of EhCAF1 and its interactions with mRNA degradation proteins including EhL-PSP endoribonuclease in cytoplasmic P-bodies. By proteomic tools they identified novel interactions between mRNA degradation proteins, which contribute to the understanding of molecular mechanisms that regulate gene expression at the posttranscriptional level in this neglected protozoan parasite. In another study, Bolaños, et al., 2014, showed the anti-amoebic effect of the flavonoid (–)-epicatechin on *E. histolytica* trophozoites, and revealed that (–)-epicatechin affects amoebic cytoskeleton proteins, resulting in alteration of important virulence mechanisms. Another important study focuses on the proteome of *Toxoplasma gondii*, the causative agent of Toxoplasmosis in animals and humans. Gomez de Leon et al., 2014, describe for the first time the physical and proteomics composition of the subpellicular cytoskeleton that is involved in motility, cell shape and entry, it is fundamental for understanding host cell invasion mechanisms. Finally, Cázarez-Raga et al., 2014,